

## RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/603, SDS  
Source: FRWD  
Date Processed by STIC: 10/20/04

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 10/20/2004

PATENT APPLICATION: US/10/603,505

TIME: 16:37:44

Input Set : A:\058820132NPUS01.ST25.txt

Output Set: N:\CRF4\10202004\J603505.raw

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3 <110> APPLICANT: Protein Design Labs, Inc.
4   Afar, et al.
6 <120> TITLE OF INVENTION: Methods of Prognosis of Prostate Cancer
8 <130> FILE REFERENCE: 05882.0132.NPUS01
10 <140> CURRENT APPLICATION NUMBER: 10/603,505
11 <141> CURRENT FILING DATE: 2003-06-24
13 <160> NUMBER OF SEQ ID NOS: 2
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1104
19 <212> TYPE: PRT
20 <213> ORGANISM: Homo sapiens
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29      20      25      30
32 Asp Leu Ser Tyr Ser Glu Ser Asp Leu Val Asn Phe Ile Gln Ala Asn
33      35      40      45
36 Phe Lys Lys Arg Glu Cys Val Phe Phe Thr Lys Asp Ser Lys Ala Thr
37      50      55      60
40 Glu Asn Val Cys Lys Cys Gly Tyr Ala Gln Ser Gln His Met Glu Gly
41 65      70      75      80
44 Thr Gln Ile Asn Gln Ser Glu Lys Trp Asn Tyr Lys Lys His Thr Lys
45      85      90      95
48 Glu Phe Pro Thr Asp Ala Phe Gly Asp Ile Gln Phe Glu Thr Leu Gly
49      100     105     110
52 Lys Lys Gly Lys Tyr Ile Arg Leu Ser Cys Asp Thr Asp Ala Glu Ile
53      115     120     125
56 Leu Tyr Glu Leu Leu Thr Gln His Trp His Leu Lys Thr Pro Asn Leu
57      130     135     140
60 Val Ile Ser Val Thr Gly Gly Ala Lys Asn Phe Ala Leu Lys Pro Arg
61 145     150     155     160
64 Met Arg Lys Ile Phe Ser Arg Leu Ile Tyr Ile Ala Gln Ser Lys Gly
65      165     170     175
68 Ala Trp Ile Leu Thr Gly Gly Thr His Tyr Gly Leu Met Lys Tyr Ile
69      180     185     190
72 Gly Glu Val Val Arg Asp Asn Thr Ile Ser Arg Ser Ser Glu Glu Asn
73      195     200     205
76 Ile Val Ala Ile Gly Ile Ala Ala Trp Gly Met Val Ser Asn Arg Asp
77      210     215     220
80 Thr Leu Ile Arg Asn Cys Asp Ala Glu Gly Tyr Phe Leu Ala Gln Tyr
81 225     230     235     240

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84 Leu Met Asp Asp Phe Thr Arg Asp Pro Leu Tyr Ile Leu Asp Asn Asn
85           245           250           255
88 His Thr His Leu Leu Leu Val Asp Asn Gly Cys His Gly His Pro Thr
89           260           265           270
92 Val Glu Ala Lys Leu Arg Asn Gln Leu Glu Lys Tyr Ile Ser Glu Arg
93           275           280           285
96 Thr Ile Gln Asp Ser Asn Tyr Gly Gly Lys Ile Pro Ile Val Cys Phe
97           290           295           300
100 Ala Gln Gly Gly Gly Lys Glu Thr Leu Lys Ala Ile Asn Thr Ser Ile
101 305           310           315           320
104 Lys Asn Lys Ile Pro Cys Val Val Val Glu Gly Ser Gly Gln Ile Ala
105           325           330           335
108 Asp Val Ile Ala Ser Leu Val Glu Val Glu Asp Ala Leu Thr Ser Ser
109           340           345           350
112 Ala Val Lys Glu Lys Leu Val Arg Phe Leu Pro Arg Thr Val Ser Arg
113           355           360           365
116 Leu Pro Glu Glu Glu Thr Glu Ser Trp Ile Lys Trp Leu Lys Glu Ile
117           370           375           380
120 Leu Glu Cys Ser His Leu Leu Thr Val Ile Lys Met Glu Glu Ala Gly
121 385           390           395           400
124 Asp Glu Ile Val Ser Asn Ala Ile Ser Tyr Ala Leu Tyr Lys Ala Phe
125           405           410           415
128 Ser Thr Ser Glu Gln Asp Lys Asp Asn Trp Asn Gly Gln Leu Lys Leu
129           420           425           430
132 Leu Leu Glu Trp Asn Gln Leu Asp Leu Ala Asn Asp Glu Ile Phe Thr
133           435           440           445
136 Asn Asp Arg Arg Trp Glu Ser Ala Asp Leu Gln Glu Val Met Phe Thr
137           450           455           460
140 Ala Leu Ile Lys Asp Arg Pro Lys Phe Val Arg Leu Phe Leu Glu Asn
141 465           470           475           480
144 Gly Leu Asn Leu Arg Lys Phe Leu Thr His Asp Val Leu Thr Glu Leu
145           485           490           495
148 Phe Ser Asn His Phe Ser Thr Leu Val Tyr Arg Asn Leu Gln Ile Ala
149           500           505           510
152 Lys Asn Ser Tyr Asn Asp Ala Leu Leu Thr Phe Val Trp Lys Leu Val
153           515           520           525
156 Ala Asn Phe Arg Arg Gly Phe Arg Lys Glu Asp Arg Asn Gly Arg Asp
157           530           535           540
160 Glu Met Asp Ile Glu Leu His Asp Val Ser Pro Ile Thr Arg His Pro
161 545           550           555           560
164 Leu Gln Ala Leu Phe Ile Trp Ala Ile Leu Gln Asn Lys Lys Glu Leu
165           565           570           575
168 Ser Lys Val Ile Trp Glu Gln Thr Arg Gly Cys Thr Leu Ala Ala Leu
169           580           585           590
172 Gly Ala Ser Lys Leu Leu Lys Thr Leu Ala Lys Val Lys Asn Asp Ile
173           595           600           605
176 Asn Ala Ala Gly Glu Ser Glu Glu Leu Ala Asn Glu Tyr Glu Thr Arg
177           610           615           620
180 Ala Val Glu Leu Phe Thr Glu Cys Tyr Ser Ser Asp Glu Asp Leu Ala

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181 625          630          635          640
184 Glu Gln Leu Leu Val Tyr Ser Cys Glu Ala Trp Gly Gly Ser Asn Cys
185          645          650          655
188 Leu Glu Leu Ala Val Glu Ala Thr Asp Gln His Phe Ile Ala Gln Pro
189          660          665          670
192 Gly Val Gln Asn Phe Leu Ser Lys Gln Trp Tyr Gly Glu Ile Ser Arg
193          675          680          685
196 Asp Thr Lys Asn Trp Lys Ile Leu Cys Leu Phe Ile Ile Pro Leu
197          690          695          700
200 Val Gly Cys Gly Phe Val Ser Phe Arg Lys Lys Pro Val Asp Lys His
201 705          710          715          720
204 Lys Lys Leu Leu Trp Tyr Tyr Val Ala Phe Phe Thr Ser Pro Phe Val
205          725          730          735
208 Val Phe Ser Trp Asn Val Val Phe Tyr Ile Ala Phe Leu Leu Leu Phe
209          740          745          750
212 Ala Tyr Val Leu Leu Met Asp Phe His Ser Val Pro His Pro Pro Glu
213          755          760          765
216 Leu Val Leu Tyr Ser Leu Val Phe Val Leu Phe Cys Asp Glu Val Arg
217          770          775          780
220 Gln Trp Tyr Val Asn Gly Val Asn Tyr Phe Thr Asp Leu Trp Asn Val
221 785          790          795          800
224 Met Asp Thr Leu Gly Leu Phe Tyr Phe Ile Ala Gly Ile Val Phe Arg
225          805          810          815
228 Leu His Ser Ser Asn Lys Ser Ser Leu Tyr Ser Gly Arg Val Ile Phe
229          820          825          830
232 Cys Leu Asp Tyr Ile Ile Phe Thr Leu Arg Leu Ile His Ile Phe Thr
233          835          840          845
236 Val Ser Arg Asn Leu Gly Pro Lys Ile Ile Met Leu Gln Arg Met Leu
237          850          855          860
240 Ile Asp Val Phe Phe Phe Leu Phe Leu Phe Ala Val Trp Met Val Ala
241 865          870          875          880
244 Phe Gly Val Ala Arg Gln Gly Ile Leu Arg Gln Asn Glu Gln Arg Trp
245          885          890          895
248 Arg Trp Ile Phe Arg Ser Val Ile Tyr Glu Pro Tyr Leu Ala Met Phe
249          900          905          910
252 Gly Gln Val Pro Ser Asp Val Asp Gly Thr Thr Tyr Asp Phe Ala His
253          915          920          925
256 Cys Thr Phe Thr Gly Asn Glu Ser Lys Pro Leu Cys Val Glu Leu Asp
257          930          935          940
260 Glu His Asn Leu Pro Arg Phe Pro Glu Trp Ile Thr Ile Pro Leu Val
261 945          950          955          960
264 Cys Ile Tyr Met Leu Ser Thr Asn Ile Leu Leu Val Asn Leu Leu Val
265          965          970          975
268 Ala Met Phe Gly Tyr Thr Val Gly Thr Val Gln Glu Asn Asn Asp Gln
269          980          985          990
272 Val Trp Lys Phe Gln Arg Tyr Phe Leu Val Gln Glu Tyr Cys Ser Arg
273          995          1000          1005
276 Leu Asn Ile Pro Phe Pro Phe Ile Val Phe Ala Tyr Phe Tyr Met
277          1010          1015          1020

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281      1025                      1030                      1035
284 Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp Asn Glu Thr Leu
285      1040                      1045                      1050
288 Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val Lys Ile Asn
289      1055                      1060                      1065
292 Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg Phe Arg
293      1070                      1075                      1080
296 Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys Glu
297      1085                      1090                      1095
300 Ile Ala Asn Lys Ile Lys
301      1100
304 <210> SEQ ID NO: 2
305 <211> LENGTH: 3315
306 <212> TYPE: DNA
307 <213> ORGANISM: Homo sapiens
309 <400> SEQUENCE: 2
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314 ttggtgaatt ttattcaagc aaattttaag aaacgagaat gtgtcttctt taccaaagat      180
316 tccaaggcca cggagaatgt gtgcaagtgt ggctatgccc agagccagca catggaaggc      240
318 acccagatca accaaagtga gaaatggaac tacaagaaac acaccaagga atttcctacc      300
320 gacgcctttg gggatattca gtttgagaca ctgggggaaga aagggaagta tatacgtctg      360
322 tcttgcgaca cggacgcgga aatcctttac gagctgctga ccagcactg gcacctgaaa      420
324 acaccaacc tggtcatttc tgtgaccggg ggcgccaaga acttcgccct gaagccgcgc      480
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330 atcagcagga gttcagagga gaattattgt gccattggca tagcagcttg gggcatggtc      660
332 tccaaccggg acaccctcat caggaattgc gatgctgagg gctatttttt agcccagtac      720
334 cttatggatg acttcacaag agatccactg tatatcctgg acaacaacca cacacatttg      780
336 ctgctcgttg acaatggctg tcatggacat cccactgtcg aagcaaagct ccggaatcag      840
338 ctagagaagt atatctctga gcgcactatt caagattcca actatggtgg caagatcccc      900
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368 tgggagcaga ccaggggctg cactctggca gccctgggag ccagcaagct tctgaagact      1800
370 ctggccaaag tgaagaacga catcaatgct gctggggagt ccgaggagct ggctaattag      1860
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376 gtggaggcca cagaccagca ttcatcgcc cagcctgggg tccagaattt tctttctaag 2040
378 caatggatatg gagagatttc ccgagacacc aagaactgga agattatcct gtgtctgttt 2100
380 attataccct tgggtgggctg tggctttgta tcatttagga agaaacctgt cgacaagcac 2160
382 aagaagctgc tttggtacta tgtggcggtc ttcacctccc ccttcgtggg cttctcctgg 2220
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386 cattcggtgc cacaccccc cgagctggtc ctgtactcgc tggctcttgt cctcttctgt 2340
388 gatgaagtga gacagtggta cgtaaattgg gtgaattatt ttactgacct gtggaatgtg 2400
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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/603,505

DATE: 10/20/2004

TIME: 16:37:45

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